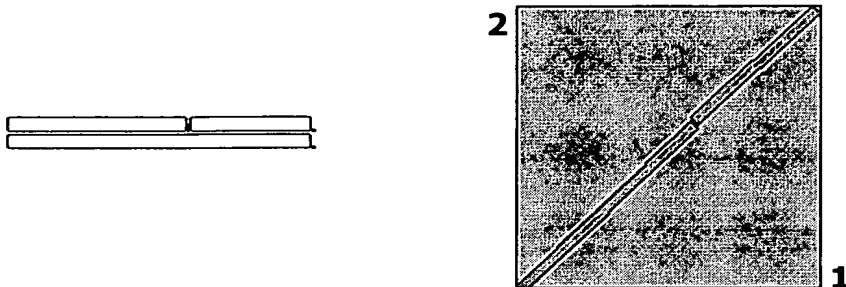


# BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [N v-16-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ Align

**Sequence 1** lcl|seq\_1 **Length** 101 (1 .. 101)

**Sequence 2** lcl|seq\_2 **Length** 102 (1 .. 102)



**NOTE:**The statistics (bitscore and expect value) is calculated based on the size of nr database

Score =, 147 bits (371), Expect = 4e -35  
Identities = 61/101 (60%), Positives = 80 /101 (78%), Gaps = 1/101 (0%)

```
Query: 1   CKRHPLYVDFSDVGWNDWIVAPPGYHAFYC HGECPFPLADHLNSTNHAIVQTLVNSVNSK 60
          CK+H LYV F D+GW DWI+AP GY A+YC GEC FPL ++N+TNHAIVQTLV+ +N +
Sbjct: 1   CKKHELYVSFRDLGWQDWIIAPEGYAAYYC EGECAPPLNSYMNATNHAIVQTLVHFINPE 60

Query: 61  -IPKACCVPTELSAISMLYLDENEKVVLKQDMVVEGCGC 100
          +PK CC PT+L+AIS+LY D++ V+LK Y++MVV CGC
Sbjct: 61  TVPKPCCAPTQLNAISVLYFDDSSNVILKK YRNMVVRACGC 101
```

CPU time: 0.03 user secs. 0.04 sys. secs 0.07 total secs.

Lambda	K	H
0.323	0.139	0.470

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 133

Number of Sequences: 0

Number of extensions: 3

Number of successful extensions: 2

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in pr elim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non -prelim): 1

length of query: 101

length of database: 463,002,162  
effective HSP length: 77  
effective length of query: 24  
effective length of database: 463,002,085  
effective search space: 11112050040  
effective search space used: 11112050040  
T: 9  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 41 (21.9 bits)  
S2: 67 (30.4 bits)